2005

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RESULT 1
US-10-071-174A-1-COPY
Sequence 1, Application US/10071174A
; GENERAL INFORMATION:
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Listing first 45 summaries
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NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn versior
SEQ ID NO 1
LENGTH: 887
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                    TITLE OF INVENTION: APOPTOSIS MODULATOR BCI
TITLE OF INVENTION: SAME
FILE REFERENCE: 8014-014-US
CURRENT APPLICATION NUMBER: US/10/071,174A
CURRENT FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/267,166
PRIOR APPLICATION NUMBER: 60/267,166
PRIOR FILING DATE: 2001-02-07
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APPLICANT: Reed, John C.
APPLICANT: Ke, Ning
APPLICANT: Adam, Godzik
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RESULT 2
US-10-071-174A-37-COPY
US-10-071-174A-37-COPY
Sequence 37, Application US/10071174A

GENERAL INFORMATION:

APPLICANT: The Burnham Institute
APPLICANT: Reed, John C.

APPLICANT: Reed, John C.

APPLICANT: Adam, Godzik

APPLICANT: Adam, Godzik

TITLE OF INVENTION: APOPTOSIS MODULATOR BCL-B AND METHODS FOR MAKING AND USING
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Query Match

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; ORGANISM: Homo sapiens
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SEQ ID NO 37
LENGTH: 130
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FILE REFERENCE: 8014-014-US
CURRENT APPLICATION NUMBER: US/10/071,174A
CURRENT FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/267,166
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 37
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CURRENT FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/267,166
PRIOR FILING DATE: 2001-02-07
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ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: 60/267,166
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APPLICANT: Adam, Godzik
TITLE OF INVENTION: APOPTOSIS MODULATOR BCL-B AND METHODS FOR MAKING AND USING THE
TITLE OF INVENTION: SAMB
FILE REFERENCE: 8014-014-US
CURRENT APPLICATION NUMBER: US/10/071,174A
CURRENT FILING DATE: 2002-02-07
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APPLICANT: Reed, John C.
APPLICANT: Ke, Ning
APPLICANT: Adam, Godzik
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ORGANISM: Homo sapiens
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APPLICANT: Adam, Godzik
TITLE OF INVENTION: APOPTOSIS MODULATOR BCL-B ANI
TITLE OF INVENTION: SAMB
FILE REFERENCE: 8014-0.14-US
CURRENT APPLICATION UMBER: US/10/071,174A
CURRENT FILING DATE: 2002-02-07
PRIOR FILING DATE: 2001-02-07
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                                                                                                                                  SOFTWARE: PatentIn version 3.3
SEQ ID NO 37
LENGTH: 130
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LENGTH: 887
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37, Application US/10071174A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: The Burnham Institute APPLICANT: Reed, John C.
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                                                                                                                     TYPE: DNA
                                                                                           ORGANISM: Homo sapiens
                                                                            FEATURE:
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mes 127; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGACGCTGCT 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGACGCTGCT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCGCCTACCTCGGCTACCCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCC 301
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Pred. No. 0;
0; Mismatches
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RESULT 4
US-10-071-174A-1-COPY/c
Sequence 1, Application US/10071174A
GENERAL INFORMATION:
APPLICANT: The Burnham Institute
APPLICANT: Reed, John C.
APPLICANT: Ke, Ning
APPLICANT: Adam, Godzik
TITLE OF INVENTION: APOPYOSIS MODULATOR BCL-B AND METHODS FOR MAKING AND USING THE
TITLE OF INVENTION: SAME
FILE REFERENCE: 8014-014-US
CURRENT APPLICATION NUMBER: US/10/071,174A
CURRENT FILING DATE: 2002-07
PRIOR APPLICATION NUMBER: 60/267,166
PRIOR FILING DATE: 2001-02-07
INUMBER OF SEQ ID NOS: 37
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 1
LENGTH: 887
TYPE: DNA
ORGANISM: Homo sapiens
US-10-071-174A-1-COPY
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Search completed: June 6, 2005, 09:08:24 Job time: 0.127827 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 19.4%; Score 25.2; DB 1; Length 130; Best Local Similarity 58.3%; Pred. No. 0; Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps
                                                                                           271 GCGGT 267
                                                                                                                                                                                                 331 CCAGGTGGGGCCGGGGCTGTCGGAGAGCACGGAATCCGCCATCAGCGCCACCAGCTCGAA 272
                                                                                                                                                                                                                        33 CGAGCTGGTGGCGGTGATGGCGGATTCCGTGCTCTCCGACAGCCCCGGCCCCACCTGGGA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 CCTGGGAGNAGT 97
                                                                                                                                              93 GNAGT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 ACTNETECCAGGTGGGGCCGGGGCTGTCGGAGAGCACGGAATCCGCCATCAGCGCCACCA 38
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